

## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 80.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:29:11 ; Search time 1552.5 Seconds  
(without alignments)  
572.596 Million cell updates/sec

Title: US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagaatggtgacgctaata 19

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_hic:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_est7:\*
- 9: gb\_gss1:\*
- 10: gb\_gss2:\*
- 11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					

No matches found

Search completed: February 5, 2006, 13:07:28  
Job time : 1552.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 10:42:21 ; Search time 894 Seconds  
(without alignments)  
1208.082 Million cell updates/sec

Title: US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagaatggtgacgctaata 19

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vi:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
-----						

No matches found

Search completed: February 5, 2006, 12:01:29  
Job time : 894 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 07:35:28 ; Search time 218.5 Seconds  
(without alignments)  
579.538 Million cell updates/sec

**Title:** US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagaatggtgacgcta 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 19

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 19

### Post-processing: Listing first 100 summaries

Database : N Geneseq 21:★

```

1: 1: geneseqn1980s:*
2: 2: geneseqn1990s:*
3: 3: geneseqn2000s:*
4: 4: geneseqn2001as:*
5: 5: geneseqn2001bs:*
6: 6: geneseqn2002as:*
7: 7: geneseqn2002bs:*
8: 8: geneseqn2003as:*
9: 9: geneseqn2003bs:*
10: 10: geneseqn2003cs:*
11: 11: geneseqn2003ds:*
12: 12: geneseqn2004as:*
13: 13: geneseqn2004bs:*
14: 14: geneseqn2005s:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19	100.0	19	13	ADT26144	Adt26144 siRNA C f

## ALIGNMENTS

RESULT 1  
ADT26144  
ID ADT26144 standard; RNA; 19 BP.

AC ADT26144;

DT 27-JAN-2005 (first entry)

DE siRNA C for potassium channel subunit Kv3.4.

RNA interference; gene silencing; ds; potassium channel;  
KW  
fast spiking neuron; Parkinson's disease; Kv3.4; neuronal ion channel;  
KW  
siRNA; small interfering RNA; neurological condition; epilepsy; hearing;  
KW

learning and memory disorder.

**Rattus rattus.**

US2004220082-A1.

04-NOV-2004.

21-JAN-2004; 2004US-00761557.

21-JAN-2003; 2003US-0441375P.

(NOUN ) UNIV NORTHWESTERN.

Surmeier DJ, Tkatch T, Baranauskas G:

WPI; 2004-774947/76.

Inhibiting the ability of a fast-spiking neuronal cell to discharge at a high rate by inhibiting Kv3.4 activity, useful for treating Parkinson's disease and other neurological conditions.

Example 6; SEQ ID NO 3; 27pp; English.

The invention relates to inhibiting the ability of a fast-spiking neuronal cell to discharge at a high rate comprising providing a compound capable of inhibiting Kv3.4 activity (potassium channel subunit) to a cell expressing Kv3 channels comprising a Kv3.4 subunit (especially the Kv3.4a subunit), where the high rate of discharge is inhibited. Also included are a method of manipulating neuronal ion channels (comprising transfecting a fast-spiking neuronal cell with a vector encoding an siRNA (small interfering RNA) directed against an mRNA encoding a Kv3.4 protein where the siRNA is capable of inhibiting Kv3.4 expression in the cell), a composition comprising an siRNA construct capable of inhibiting expression of a Kv3.4 subunit in a neuronal cell and a method for screening for compounds that inhibit the activity of a Kv3.4 protein (comprising providing a cell expressing Kv3.4 protein, and a test compound, and detecting the activity of the Kv3.4 protein in the presence of the test compound). The method is useful for manipulating ion channels, in particular for treating Parkinson's disease and other neurological conditions, such as epilepsy, hearing, learning and memory disorders. The present sequence is an siRNA targeting nucleotides 1626-1644 (relative to the start codon) of the rat Kv3.4 mRNA.

Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 13; Length 19;

Best Local Similarity 100.0%; Pred. No. 0.077;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGATGGTGACGCTAAT 19

Db 1 GCAGAAATGGTGACGCTAAT 19

Search completed: February 5, 2006, 11:31:35  
Job time : 218.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 10:56:01 ; Search time 72 Seconds  
(without alignments)  
469.079 Million cell updates/sec

Title: US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagaatggtgacgctaata 19

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : Issued Patents NA:\*

1:	/cgn2_6/ptodata/1/ina/1 COMB.seq:*
2:	/cgn2_6/ptodata/1/ina/5 COMB.seq:*
3:	/cgn2_6/ptodata/1/ina/6A COMB.seq:*
4:	/cgn2_6/ptodata/1/ina/6B COMB.seq:*
5:	/cgn2_6/ptodata/1/ina/H COMB.seq:*
6:	/cgn2_6/ptodata/1/ina/FCRUS COMB.seq:*
7:	/cgn2_6/ptodata/1/ina/PP COMB.seq:*
8:	/cgn2_6/ptodata/1/ina/RE COMB.seq:*
9:	/cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

§					
Result	Query	Match	Length	ID	Description
No.	Score				
-----					
No matches found					

Search completed: February 5, 2006, 12:04:00  
Job time : 72 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:21:57 ; Search time 344.5 Seconds  
(without alignments)  
456.076 Million cell updates/sec

**Title:** US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagaatgggtgacqcta 19

Scoring table: OLIGO NUC

Scoring scale: 0-100 - noc  
Gapop\_60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 19

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length:	19
Maximum DB seq length:	19

Post-processing: Listing first 100 summaries

Database : Published Applications NA Main:\*

```

1: /cgn2_6/prodata/1/pubnpna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/1/pubnpna/US08_PUBCOMB.seq.*
3: /cgn2_6/prodata/1/pubnpna/US09_PUBCOMB.seq.*
4: /cgn2_6/prodata/1/pubnpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/prodata/1/pubnpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/prodata/1/pubnpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/prodata/1/pubnpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/prodata/1/pubnpna/US10E_PUBCOMB.seq.*
9: /cgn2_6/prodata/1/pubnpna/US11_PUBCOMB.seq.*
10: /cgn2_6/prodata/1/pubnpna/US11B_PUBCOMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19	100.0	19	8	US-10-761-557-3	Sequence 3, Appli

## ALIGNMENTS

```

RESULT 1
US-10-761-557-3
; Sequence 3, Application US/10761557
; Publication No. US20040220082A1
; GENERAL INFORMATION:
; APPLICANT: Surmeier, D. James
; APPLICANT: Tkatch, Tatiana
; APPLICANT: Baranaukas, Gytis
; TITLE OF INVENTION: Manipulation of Neuronal Ion Channels
; FILE REFERENCE: NWESTERN-08739
; CURRENT APPLICATION NUMBER: US/10/761,557
; CURRENT FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:31:41 ; Search time 184 Seconds  
(without alignments)  
86.540 Million cell updates/sec

Title: US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagaatggtgacgctaata 19

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 6068529 seqs, 419036697 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : Published Applications NA\_New.\*  
1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq1.\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq2.\*  
10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3.\*  
11: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: February 5, 2006, 13:13:41  
Job time : 184 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:29:11 ; Search time 1552.5 Seconds  
(without alignments)  
572.596 Million cell updates/sec

Title: US-10-761-557-4  
Perfect score: 19  
Sequence: 1 ggcagtggtgagccgaac 19

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hlc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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No matches found

Search completed: February 5, 2006, 13:07:28  
Job time : 1552.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 10:42:21 ; Search time 894 Seconds  
(without alignments)  
1208.082 Million cell updates/sec

Title: US-10-761-557-4

Perfect score: 19

Sequence: 1 ggcagtggtgagccgaaac 19

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				
Result	Query			
No.	Score	Match	Length	DB ID Description
-----				

No matches found

Search completed: February 5, 2006, 12:01:29  
Job time : 894 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 07:35:28 ; Search time 218.5 Seconds  
(without alignments)  
579.538 Million cell updates/sec

Title: US-10-761-557-4

Perfect score: 19  
Sequence: 1 ggcagtggtgagccgaac 19

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 332346308 residues

Word size : 19

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

- Database : N\_Geneseq\_21:\*
- 1: Geneseqn1980s.\*
  - 2: Geneseqn1990s.\*
  - 3: Geneseqn2000s.\*
  - 4: Geneseqn2001as.\*
  - 5: Geneseqn2001bs.\*
  - 6: Geneseqn2002as.\*
  - 7: Geneseqn2002bs.\*
  - 8: Geneseqn2003as.\*
  - 9: Geneseqn2003bs.\*
  - 10: Geneseqn2003cs.\*
  - 11: Geneseqn2003ds.\*
  - 12: Geneseqn2004as.\*
  - 13: Geneseqn2004bs.\*
  - 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	19	100.0	19	13	ADT26145	Adt26145 siRNA D f

ALIGNMENTS

RESULT 1  
ADT26145  
ID ADT26145 standard; RNA; 19 BP.  
XX  
AC ADT26145;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE siRNA D for potassium channel subunit Kv3.4.  
XX  
KW RNA interference; gene silencing; ds; potassium channel;  
KW fast spiking neuron; Parkinson's disease; Kv3.4; neuronal ion channel;  
KW siRNA; small interfering RNA; neurological condition; epilepsy; hearing;

KW learning and memory disorder.  
XX  
OS Rattus rattus.  
XX  
PN US2004220082-A1.  
XX  
PD 04-NOV-2004.  
XX  
PF 21-JAN-2004; 2004US-00761557.  
XX  
PR 21-JAN-2003; 2003US-0441375P.  
XX  
PA (NOUN ) UNIV NORTHWESTERN.  
XX  
PI Surmeier DJ, Tkatch T, Baranauskas G;  
XX WPI; 2004-774947/76.  
XX  
PT Inhibiting the ability of a fast-spiking neuronal cell to discharge at a  
PT high rate by inhibiting Kv3.4 activity, useful for treating Parkinson's  
PT disease and other neurological conditions.  
XX  
PS Example 6; SEQ ID NO 4; 27pp; English.  
XX  
CC The invention relates to inhibiting the ability of a fast-spiking  
CC neuronal cell to discharge at a high rate comprising providing a compound  
CC capable of inhibiting Kv3.4 activity (potassium channel subunit) to a  
CC cell expressing Kv3 channels comprising a Kv3.4 subunit (especially the  
CC Kv3.4a subunit), where the high rate of discharge is inhibited. Also  
CC included are a method of manipulating neuronal ion channels (comprising  
CC transfecting a fast-spiking neuronal cell with a vector encoding an siRNA  
CC (small interfering RNA) directed against an mRNA encoding a Kv3.4 protein  
CC where the siRNA is capable of inhibiting Kv3.4 expression in the cell), a  
CC composition comprising an siRNA construct capable of inhibiting  
CC expression of a Kv3.4 subunit in a neuronal cell and a method for  
CC screening for compounds that inhibit the activity of a Kv3.4 protein  
CC (comprising providing a cell expressing Kv3.4 protein, and a test  
CC compound, and detecting the activity of the Kv3.4 protein in the presence  
CC of the test compound). The method is useful for manipulating ion  
CC channels, in particular for treating Parkinson's disease and other  
CC neurological conditions, such as epilepsy, hearing, learning and memory  
CC disorders. The present sequence is an siRNA targeting nucleotides 11825-  
CC 1843 (relative to the start codon) of the rat Kv3.4 mRNA.  
XX  
SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 19; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGCAGTGTGAGCCGAAAC 19  
Db 1 GGCAGTGTGAGCCGAAAC 19  
Search completed: February 5, 2006, 11:31:35  
Job time : 218.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 10:56:01 ; Search time 72 Seconds  
(without alignments)  
469.079 Million cell updates/sec

Title: US-10-761-557-4  
Perfect score: 19  
Sequence: 1 ggcagtgttgagccgaac 19  
Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/PP COMB.seq:  
7: /cgn2\_6/ptodata/1/ina/RE COMB.seq:  
8: /cgn2\_6/ptodata/1/ina/backfiles1.seq:  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
-----					

No matches found

Search completed: February 5, 2006, 12:04:00  
Job time : 72 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:21:57 ; Search time 344.5 Seconds  
(without alignments)  
456.076 Million cell updates

**Title:** US-10-761-557-4

Perfect score: 19

Sequence: 1 ggcagtgttgagccgaac 19

Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 19

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length:	19
Maximum DB seq length:	19

Post-processing: Listing first 100 summaries

Database : Published Applications NA Main:\*

```

1: /cgn2_6/prodata/1/pubnpna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/1/pubnpna/US08_PUBCOMB.seq.*
3: /cgn2_6/prodata/1/pubnpna/US09_PUBCOMB.seq.*
4: /cgn2_6/prodata/1/pubnpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/prodata/1/pubnpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/prodata/1/pubnpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/prodata/1/pubnpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/prodata/1/pubnpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/prodata/1/pubnpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/prodata/1/pubnpna/US11_PUBCOMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	8	US-10-761-557-4
					Sequence 4, Appli

## ALIGNMENTS

```

RESULT 1
US-10-761-557-4
; Sequence 4, Application US/10761557
; Publication NO. US20040220082A1
; GENERAL INFORMATION:
; APPLICANT: Surmeier, D. James
; APPLICANT: Tkatch, Tatiana
; APPLICANT: Baranaukas, Gytis
; TITLE OF INVENTION: Manipulation of Neuronal Ion Channels
; FILE REFERENCE: NWESTERN-08739
; CURRENT APPLICATION NUMBER: US/10/761,557
; CURRENT FILING DATE: 2004-01-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:31:41 ; Search time 184 Seconds  
(without alignments)  
86.540 Million cell updates/sec

Title: US-10-761-557-4  
Perfect score: 19  
Sequence: 1 ggcagtggtgagccgaac 19  
Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 6088529 seqs, 419036697 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
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Post-processing: Listing first 100 summaries

Database : Published Applications\_NA\_New.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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No matches found

Search completed: February 5, 2006, 13:13:41  
Job time : 184 secs

**LOCUS** RRPCP2858 2858 bp mRNA linear ROD 14-JAN-1993  
**DEFINITION** R.rattus mRNA for potassium channel protein (2858 bp).  
**ACCESSION** X62841  
**VERSION** X62841.1 GI:57648  
**KEYWORDS** voltage-gated potassium channel.  
**SOURCE** Rattus rattus (black rat)  
**ORGANISM** Rattus rattus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Rattus.  
**REFERENCE** 1 (bases 1 to 2858)  
**AUTHORS** Retting, J., Wunder, F., Stocker, M., Lichtinghagen, R., Mastiaux, F.,  
 Beckh, S., Kues, W., Pedarzani, P., Schroeter, K.H., Ruppersberg, J.P.,  
 Veh, R. and Pongs, O.  
**TITLE** Characterization of a Shaw-related potassium channel family in rat  
 brain  
**JOURNAL** EMBO J. 11 (7), 2473-2486 (1992)  
**PUBMED** 1378192  
**REFERENCE** 2 (bases 1 to 2858)  
**AUTHORS** Pongs, O.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (22-OCT-1991) O. Pongs, Zentrum f Molekulare  
 Neurobiologie, ZMNH Haus 42, Martinistr 52, 2000 Hamburg 20, FRG  
**FEATURES** Location/Qualifiers  
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